

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) An isolated or purified peptide ~~comprising~~ with an amino acid sequence selected from the group consisting of:
 - (a) GPRGPPGPPGKPGDDGEAGKPGKSGERGPPGPQGARGFPGTPGLPGVK GHRGYPLDGAKEAGAPGVKGESGSPGQNGSPGGPM (CB12) (SEQ ID NO: 11);
 - (b) GPRGPPGPPGKPGDDGEAGKPGKSGERGPPG (CB12-I) (SEQ ID NO: 2);
 - (c) ERGPPGPQGARGFPGTPGLPGVK (CB12-II) (SEQ ID NO: 3);
 - (d) GLPGVKGHRGYPLDGAKEAGAPG (CB12-III) (SEQ ID NO: 4);
 - (e) GEAGAPGVKGESGSPGQNGSPGPM (CB12-IV) (SEQ ID NO: 5);
 - (f) GERGPPGPQGARGFP*GTP*GLP*GVK (SEQ ID NO: 6) wherein the * denotes sites of hydroxylation. (Pro6);
 - (g) GERGPP*GPQGARGFPGTP*GLP*GVK (SEQ ID NO: 7) wherein the * denotes sites of hydroxylation. (Pro15);
 - (h) GERGPP*GPQGARGFP*GTPGLP*GVK (SEQ ID NO: 8) wherein the * denotes sites of hydroxylation. (Pro18); ~~and~~ or
 - (i) GERGPP*GPQGARGFP*GTP*GLPGVK (SEQ ID NO: 9) wherein the * denotes sites of hydroxylation. (Pro21);

~~or a fragment or conservatively substituted variant thereof~~, wherein said peptide is effective in altering decreasing the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.

2. (Currently Amended) ~~The~~ An isolated or purified peptide ~~fragment~~ of claim 1, wherein said peptide is further modified by hydroxylation.

3. (Currently Amended) ~~The~~ An isolated or purified peptide ~~fragment~~ of claim 2, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of said peptide.

4. (Currently Amended) ~~The~~ An isolated or purified peptide ~~fragment~~ of claim 3, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

5. (Currently Amended) ~~The~~ An isolated or purified peptide ~~fragment~~ of claim 3, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

6. (Currently Amended) A peptide ~~fragment~~ consisting essentially of an amino acid sequence denoted CB12:

GPRGPPGPPGKPGDDGEAGKPGKSGERGPPGPQGARGFPGTPGLPGVKGHRGYPL
DGAKEAGAPGVKGESGSPGQNGSPGGPM (SEQ ID NO: 11).

7. (Currently Amended) The peptide ~~fragment~~ of claim 6, wherein said peptide is further modified by hydroxylation.

8. (Currently Amended) The peptide ~~fragment~~ of claim 7, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of the peptide.

9. (Currently Amended) The peptide ~~fragment~~ of claim 8, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

10. (Currently Amended) The peptide ~~fragment~~ of claim 8, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

11. (Currently Amended) The peptide ~~fragment~~ of claim 7, wherein said peptide consists essentially of
GPRGPP*GPP*GKP*GDDGEAGKP*GKSGERGPP*GPQGARGFP*GTP*GLP*GVKGH
RGYPGLDGAKEAGAP*GVKGESGSP*GQNGSP*GGPM (SEQ ID NO: 12) and
wherein the * denotes sites of hydroxylation.

12 - 15 (**Canceled**)

16. (Currently Amended) A peptide ~~fragment~~ consisting essentially of an amino acid sequence denoted CB12-II: GERGPPGPQGARGFPGLPGVK (SEQ ID NO: 13).

17. (Currently Amended) The peptide ~~fragment~~ of claim 16, wherein said peptide is further modified by hydroxylation.

18. (Currently Amended) The peptide ~~fragment~~ of claim 17, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of the peptide.

19. (Currently Amended) The peptide ~~fragment~~ of claim 18, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

20. (Currently Amended) The peptide ~~fragment~~ of claim 18, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

21. (Currently Amended) The peptide ~~fragment~~ of claim 17, wherein said peptide consists essentially of GERGPP*GPQGARGFP*GTP*GLP*GVK (SEQ ID NO: 14).

22 - 25 (**Canceled**)

26. (Currently Amended) The peptide ~~fragment~~ of claim 16, wherein said peptide consists essentially of GERGPPGPQGARGFP*GTP*GLP*GVK (Pro6) (SEQ ID NO: 6) and wherein the * denotes sites of hydroxylation.

27 - 28 (**Canceled**)

29. (Currently Amended) The peptide ~~fragment~~ of claim 16, wherein said peptide consists essentially of GERGPP*GPQGARGFPGTP*GLP*GVK (Pro15) (SEQ ID NO: 7) and wherein the * denotes sites of hydroxylation.

30 - 31 (**Canceled**)

32. (Currently Amended) The peptide ~~fragment~~ of claim 16, wherein said peptide consists essentially of GERGPP*GPQGARGFP*GTPGLP*GVK (Pro18) (SEQ ID NO: 8) and wherein the * denotes sites of hydroxylation.

33 - 34 (**Canceled**)

35. (Currently Amended) The peptide ~~fragment~~ of claim 16, wherein said peptide consists essentially of GERGPP*GPQGARGFP*GTP*GLPGVK (Pro21) (SEQ ID NO: 9) and wherein the * denotes sites of hydroxylation.

36 - 37 (**Canceled**)

38. (Currently Amended) A peptide ~~fragment~~ consisting essentially of an amino acid sequence denoted as CB12-I: GPRGPPGPPGKPGDDGEAGKPGKSGERGPPG (SEQ ID NO: 2).

39. (Currently Amended) The peptide ~~fragment~~ of claim 38, wherein said peptide is further modified by hydroxylation.

40. (Currently Amended) The peptide ~~fragment~~ of claim 39, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of the peptide.

41. (Currently Amended) The peptide ~~fragment~~ of claim 40, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

42. (Currently Amended) The peptide ~~fragment~~ of claim 40, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

43. (Currently Amended) The peptide ~~fragment~~ of claim 38, wherein said peptide consists essentially of GPRGPP*GPP*GKP*GDDGEAGKP*GKSGERGPP*G (SEQ ID NO: 15) and wherein the * denotes sites of hydroxylation.

44 - 47 (**Canceled**)

48. (Currently Amended) A peptide ~~fragment~~ wherein said peptide consists essentially of an amino acid sequence denoted as CB12-III:
GLPGVKGHRGYPLDGAKEAGAPG (SEQ ID NO: 4).

49. (Currently Amended) The peptide ~~fragment~~ of claim 48, wherein said peptide is further modified by hydroxylation.

50. (Currently Amended) The peptide ~~fragment~~ of claim 49, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of the peptide.

51. (Currently Amended) The peptide ~~fragment~~ of claim 50, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

52. (Currently Amended) The peptide ~~fragment~~ of claim 50, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

53. (Currently Amended) The peptide ~~fragment~~ of claim 48, wherein said peptide consists essentially of GLP*GVKGHRGYPLDGAKEAGAP*G (SEQ ID NO: 16) and wherein the * denotes sites of hydroxylation.

54 - 57 (**Canceled**)

58. (Currently Amended) A peptide ~~fragment~~ consisting essentially of an amino acid sequence denoted as CB12-IV: GEAGAPGVKGESGSPGQNGSPGPM (SEQ ID NO: 5).

59. (Currently Amended) The peptide ~~fragment~~ of claim 58, wherein said peptide is further modified by hydroxylation.

60. (Currently Amended) The peptide ~~fragment~~ of claim 59, wherein said peptide is hydroxylated at one or more of the proline or lysine residues of the peptide.

61. (Currently Amended) The peptide ~~fragment~~ of claim 60, wherein said peptide is hydroxylated at one or more proline residues located within the sequence Gly-X-Pro, where X indicates any amino acid.

62. (Currently Amended) The peptide ~~fragment~~ of claim 60, wherein said peptide is hydroxylated at one or more lysine residues located within the sequence Gly-X-Lys, where X indicates any amino acid.

63. (Currently Amended) The peptide ~~fragment~~ of claim 58, wherein said peptide consists essentially of GEAGAP*GVKGESGSP*GQNGSP*GPM (SEQ ID NO: 17) and wherein the * denotes sites of hydroxylation.

64 - 67 (**Canceled**)

68. (Currently Amended) [[A]] The peptide as in any one of claims 1, 6, 16, 38, 48 or 58, wherein 1-5 amino acids of the peptide sequence have been replaced using conservative substitutions and wherein said peptide is effective in ~~altering~~ decreasing the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.

69. (Currently Amended) [[A]] The peptide which has at least 80% ~~homology~~ sequence identity to a peptide as in any one of claims 1, 6, 16, 38, 48 or 58, and wherein said peptide is effective in ~~altering~~ decreasing the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.

70-92. (**Canceled**)

93. (New) The peptide which has at least 90% sequence identity to a peptide as in any one of claims 1, 6, 16, 38, 48 or 58, and wherein said peptide is effective in decreasing the rate of degradation of type II collagen or the rate of chondrocyte hypertrophy.

94. (New) A method of regulating collagen turnover comprising:

administering to a subject a pharmaceutically effective amount of a composition comprising a peptide of claim 1.

95. (New) A method of inhibiting chondrocyte hypertrophy in a subject comprising:

administering to said subject a pharmaceutically effective amount of a peptide of claim 1, whereby said hypertrophy is inhibited.